

1K

RAW SEQUENCE LISTING ERROR REPORT

BIOTECHNOLOGY
SYSTEMS
BRANCH



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NOV 27 2000

TECH CENTER 1600/2900

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 08/816,011B
Source: 1646
Date Processed by STIC: 11/13/2000

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin30help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:
<http://www.uspto.gov/web/offices/pac/checker>

Raw Sequence Listing Error Summary

ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER: 08/8160146

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ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 ☐ Wrapped Nucleics The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 2 ☐ Wrapped Aminos The amino acid-number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 3 ☐ Incorrect Line Length The rules require that a line not exceed 72 characters in length. This includes spaces.
- 4 ☐ Misaligned Amino Acid Numbering The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and use spacing between the numbers.
- 5 ☐ Non-ASCII This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.
- 6 ☐ Variable Length Sequence(s) ____ contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and indicate in the (ix) feature section that some may be missing.
- 7 ☐ PatentIn ver. 2.0 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies primarily to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 8 ☐ Skipped Sequences (OLD RULES) Sequence(s) ____ missing. If intentional, please use the following format for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X:
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).
- 9 ☐ Skipped Sequences (NEW RULES) Sequence(s) ____ missing. If intentional, please use the following format for each skipped sequence.
<210> sequence id number
<400> sequence id number
000
- 10 ☒ Use of n's or Xaa's (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 11 ☐ Use of <213>Organism (NEW RULES) Sequence(s) ____ are missing this mandatory field or its response.
- 12 ☐ Use of <220>Feature (NEW RULES) Sequence(s) ____ are missing the <220>Feature and associated headings.
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"
Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)
- 13 ☐ PatentIn ver. 2.0 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).
Instead, please use "File Manager" or any other means to copy file to floppy disk.

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NOV 27 2000

1646

TECH CENTER 1600/2900

Does Not Comply
Corrected Diskette Needed

RAW SEQUENCE LISTING

PATENT APPLICATION: US/08/816,011B

DATE: 11/13/2000

TIME: 13:15:25

Input Set : A:\Seq51.app

Output Set: N:\CRF3\11132000\H816011B.raw

3 <110> APPLICANT: Pausch, Mark R
 4 Price, Laura A
 6 <120> TITLE OF INVENTION: Potassium Channels, Nucleotide Sequences Encoding Them,
 7 and Methods of Using Same
 9 <130> FILE REFERENCE: 01142.0122
 11 <140> CURRENT APPLICATION NUMBER: 08/816,011B
 12 <141> CURRENT FILING DATE: 1997-03-11
 14 <160> NUMBER OF SEQ ID NOS: 64
 16 <170> SOFTWARE: PatentIn Ver. 2.1
 18 <210> SEQ ID NO: 1
 19 <211> LENGTH: 2441
 20 <212> TYPE: DNA
 21 <213> ORGANISM: Drosophila melanogaster
 23 <400> SEQUENCE: 1
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 25 cttttaaaga aaaaaaaat aataagtcaa aactacaaac cacacagcga aagcgaaag 120
 26 caacgggttc tcgcagtggt tatttttttt ttcaacaatt ttgategta gtgcgacaat 180
 27 ccgtcgagca tgcgcgcgaa tcgatggatc ctgctgctca tcttctacat atcctacctg 240
 28 atgttcgggg cggcaatcta ttaccatatt gagcacggcg aggagaagat atcgcgcgc 300
 29 gaacagcgca aggcgcaaat tgcaatcaac gaatatctgc tggaggagct ggcgcacaag 360
 30 aatacgacca cacaggatga gattcttcaa cggatctcgg attactgtga caaacgggtt 420
 31 acattgcgcg cgacatatga tgatacgccc tacacgtgga ccttctacca tgccttcttc 480
 32 ttcgccttca cgttttgcct cacygtggga tatgggaata tatcgccaac cacttcgcgc 540
 33 ggacggatga tcatgatcgc gtattcgggt attggcatcc ccgtcaatgg tatectcttt 600
 34 gccgcctcgc gcaataactt tggacgtacg ttggaagcga tctacagacg ctacaaaaag 660
 35 tacaagatgt ccacggatat gcaatgtgc ccgcgcgcgc tgggattgat caccacgggt 720
 36 gtgattgccc tgattccggg aatagctctc ttctctggtg tgccctgcgt ggggtgtcac 780
 37 ctacttcgag aactgggctt atcttccatc tcgctgtact acagctatgt gaccaccaca 840
 38 acaattggat tcggtgaacta tgtgccacca ttgggagcca accagcccaa ggagttcggc 900
 39 ggctgggttc tggctatcca gatctttgtg atcgtgtggt tcatcttctc gctgggatat 960
 40 cttgtgatga tcatgacatt tateactcgg ggcctccaga gcaagaagct ggcatactct 1020
 41 gagcagcagt tgcctcccaa cctgaaggcc acacagaatc gcatctggtc tggcgtcacc 1080
 42 aaggatgtgg gctacctcgc ggaatgctc aacgagctgt acatcttcaa agtgaagcct 1140
 43 gtgtacacgc atgtagatat cgcctacaca ctgccacggt ccaattcgtg tccggatctg 1200
 44 agcatgtacc gcgtggagcc ggctcccatc ccagccgga agagggcatt ctccgtgtgc 1260
 45 gccgacatgg ttggcgccca aaggaggcgg ggcattggtac acgccaattc cgatacggat 1320
 46 ctaaccaaac tggatcgaga gaagacattc gagacggcgg aggcgtacca ccagaccacc 1380
 47 gatttctctg ccaaggtggt caacgcactg gccacgggtg agccaccgcc ggcggaacag 1440
 48 gaagatcgcg ctctctatgg ttgctatcat ggtctctcgc actccagat cctggccagc 1500
 49 gaatggctgt tctcagcgtt caacgagttc acatcacgcg gacgtccaag agcacytgcc 1560
 50 tgcctcgatt tcaatctgga ggcacctcgc tggcagagcy agaggccact gcgttcgagc 1620
 51 cacaacgaat ggacatggag cgcgcacaac cagcagatcc agyaggcatt caaccagcgc 1680
 52 tacaagggac agcagcgtgc caacggagca gccaaactcga ccatggtcca tctggagccg 1740
 53 gatgctttgg aggagcagct gagaaacaat caccgggtgc cgttcgcgtc aagaagttct 1800
 54 ccattgccgga tggctctgga cgtctgtttc ccttccagaa gaagcaccgc tcgcaggatc 1860
 55 tggagcgcaa gttgtcgtg gtctcgggtc ccgaggggtg catctcgag gaagccagat 1920
 56 ccccgctgga ctactacatc aacacggtca cggcgccctc cagtcgaatc tatttgcyca 1980

see pp 6-7

RAW SEQUENCE LISTING

DATE: 11/13/2000

PATENT APPLICATION: US/08/816,011B

TIME: 13:15:25

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Output Set: N:\CRF3\11132000\H816011B.raw

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59 gtggagccta tcaacgcaag gcggtgctg gcaagcgccg acgcgagagc atctacaccc 2160
60 agaatacaagc cccatccgct cgcgggggca gcatgtatcc gccgaccgag cagcccttgg 2220
61 cccagatgca gatgcgacgc ggcagcttgg caaccagtgg ctctggatcg gcggccatgg 2280
62 cggcagtggc cgcgcgtcgt ggcagcctct tcccagctac agcatcgga tcacgcgtga 2340
63 cctctgctcc gcgcgaagc agcatattct cggttacctc cgaagaagat atgaatgtgc 2400
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68 <211> LENGTH: 618
69 <212> TYPE: PRT
70 <213> ORGANISM: Drosophila melanogaster
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74 1 5 10 15
76 Leu Met Phe Gly Ala Ala Ile Tyr Tyr His Ile Glu His Gly Glu Glu
77 20 25 30
79 Lys Ile Ser Arg Ala Glu Gln Arg Lys Ala Gln Ile Ala Ile Asn Glu
80 35 40 45
82 Tyr Leu Leu Glu Glu Leu Gly Asp Lys Asn Thr Thr Thr Gln Asp Glu
83 50 55 60
85 Ile Leu Gln Arg Ile Ser Asp Tyr Cys Asp Lys Pro Val Thr Leu Pro
86 65 70 75 80
88 Pro Thr Tyr Asp Asp Thr Pro Tyr Thr Trp Thr Phe Tyr His Ala Phe
89 85 90 95
91 Phe Phe Ala Phe Thr Val Cys Ser Thr Val Gly Tyr Gly Asn Ile Ser
92 100 105 110
94 Pro Thr Thr Phe Ala Gly Arg Met Ile Met Ile Ala Tyr Ser Val Ile
95 115 120 125
97 Gly Ile Pro Val Asn Gly Ile Leu Phe Ala Gly Leu Gly Glu Tyr Phe
98 130 135 140
100 Gly Arg Thr Phe Glu Ala Ile Tyr Arg Arg Tyr Lys Lys Tyr Lys Met
101 145 150 155 160
103 Ser Thr Asp Met His Tyr Val Pro Pro Gln Leu Gly Leu Ile Thr Thr
104 165 170 175
106 Val Val Ile Ala Leu Ile Pro Gly Ile Ala Leu Phe Leu Val Leu Pro
107 180 185 190
109 Cys Val Gly Val His Leu Leu Arg Glu Leu Gly Leu Ser Ser Ile Ser
110 195 200 205
112 Leu Tyr Tyr Ser Tyr Val Thr Thr Thr Thr Ile Gly Phe Gly Asp Tyr
113 210 215 220
115 Val Pro Thr Phe Gly Ala Asn Gln Pro Lys Glu Phe Gly Gly Trp Phe
116 225 230 235 240
118 Val Val Tyr Gln Ile Phe Val Ile Val Trp Phe Ile Phe Ser Leu Gly
119 245 250 255
121 Tyr Leu Val Met Ile Met Thr Phe Ile Thr Arg Gly Leu Gln Ser Lys
122 260 265 270
124 Lys Leu Ala Tyr Leu Glu Gln Gln Leu Ser Ser Asn Leu Lys Ala Thr
125 275 280 285

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RAW SEQUENCE LISTING

DATE: 11/13/2000

PATENT APPLICATION: US/08/816,011B

TIME: 13:15:25

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Output Set: N:\CRF3\11132000\H816011B.raw

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131 305      310      315      320
133 Asp Val Asp Ile Ala Tyr Thr Leu Pro Arg Ser Asn Ser Cys Pro Asp
134      325      330      335
136 Leu Ser Met Tyr Arg Val Glu Pro Ala Pro Ile Pro Ser Arg Lys Arg
137      340      345      350
139 Ala Phe Ser Val Cys Ala Asp Met Val Gly Ala Gln Arg Glu Ala Gly
140      355      360      365
142 Met Val His Ala Asn Ser Asp Thr Asp Leu Thr Lys Leu Asp Arg Glu
143      370      375      380
145 Lys Thr Phe Glu Thr Ala Glu Ala Tyr His Gln Thr Thr Asp Leu Leu
146 385      390      395      400
148 Ala Lys Val Val Asn Ala Leu Ala Thr Val Lys Pro Pro Pro Ala Glu
149      405      410      415
151 Gln Glu Asp Ala Ala Leu Tyr Gly Gly Tyr His Gly Phe Ser Asp Ser
152      420      425      430
154 Gln Ile Leu Ala Ser Glu Trp Ser Phe Ser Thr Val Asn Glu Phe Thr
155      435      440      445
157 Ser Pro Arg Arg Pro Arg Ala Arg Ala Cys Ser Asp Phe Asn Leu Glu
158      450      455      460
160 Ala Pro Arg Trp Gln Ser Glu Arg Pro Leu Arg Ser Ser His Asn Glu
161 465      470      475      480
163 Trp Thr Trp Ser Gly Asp Asn Gln Gln Ile Gln Glu Ala Phe Asn Gln
164      485      490      495
166 Arg Tyr Lys Gly Gln Gln Arg Ala Asn Gly Ala Ala Asn Ser Thr Met
167      500      505      510
169 Val His Leu Glu Pro Asp Ala Leu Glu Glu Gln Leu Arg Asn Asn His
170      515      520      525
172 Arg Val Pro Val Ala Ser Arg Ser Ser Pro Cys Arg Met Val Cys Asp
173      530      535      540
175 Val Cys Phe Pro Ser Arg Arg Ser Thr Pro Arg Arg Ile Trp Ser Ala
176 545      550      555      560
178 Ser Cys Pro Trp Ser Arg Tyr Pro Arg Val Ser Ser Arg Arg Lys Pro
179      565      570      575
181 Asp Pro Arg Trp Thr Thr Ser Thr Arg Ser Arg Arg Pro Pro Val
182      580      585      590
184 Asn Pro Ile Cys Ala Thr Asp Ala Val Arg His Arg Pro Ser Asn Arg
185      595      600      605
187 Met Ala Ala Trp Pro Ala Ala Ala Ala Gly
188      610      615
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192 <211> LENGTH: 1011
193 <212> TYPE: DNA
194 <213> ORGANISM: Caenorhabditis elegans
196 <400> SEQUENCE: 3
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RAW SEQUENCE LISTING

DATE: 11/13/2000

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TIME: 13:15:25

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Output Set: N:\CRF3\11132000\H816011B.raw

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200 atattgttct ccttgcttgg aatacctcta acactgggta ccactcgtga cttggcaggt 240
201 aaattcctat ctgaacatct tgtttggttg tatggaaact atttgaattt aaaaatcttc 300
202 atattgtcac gacatcgaaa agaacggaga gagcacgttt gtgagcacty tcacagtcac 360
203 ggaatggggc atgatatgaa tatcgaggag aaaagaattc ctgcattcct ggtattagct 420
204 attctgatat tatatacagc gtttggcggg gtctaatgtt caaaattaga gccgtgggtc 480
205 ttcttcactt cattctactg gtctctcatt acaatgacta ctgtcggggt tggcgacttg 540
206 atgcccagaa gggacggata catgtatata atattgctct atatcatttt aggtaaattt 600
207 tcaatgaaaa aaaaacaaaa attcaaaata tttttaggtc ttgcaataac tacaatgtgc 660
208 attgatttgg taggagtaca gtatatcgaa aagattcatt atttcggaag aaaaattcaa 720
209 gacgctagat ctgcattggc ggttgttaga ggaaggttag tccttgatc agaactctac 780
210 gcaaatttaa tgcaaaagcg agctcgtaac atgtcccgag aagcttttat agtggagaat 840
211 ctctatggtt ccaaacacat cataccattc ataccaactg atatccgatg tattegatat 900
212 attgatcaaa ctgccgatgc tgcaccattt tccacgtcat cgtctgcaat tgatatgcaa 960
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217 <211> LENGTH: 336
218 <212> TYPE: PRT
219 <213> ORGANISM: Drosophila melanogaster
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225 Asn Glu Val Lys Lys Asn Ala Ala Thr Glu Thr Trp Thr Phe Ser Ser
226 20 25 30
228 Ser Ile Phe Phe Ala Val Thr Val Val Thr Thr Ile Gly Tyr Gly Asn
229 35 40 45
231 Pro Val Pro Val Thr Asn Ile Gly Arg Ile Trp Cys Ile Leu Phe Ser
232 50 55 60
234 Leu Leu Gly Ile Pro Leu Thr Leu Val Thr Ile Ala Asp Leu Ala Gly
235 65 70 75 80
237 Lys Phe Leu Ser Glu His Leu Val Trp Leu Tyr Gly Asn Tyr Leu Lys
238 85 90 95
240 Leu Lys Tyr Leu Ile Leu Ser Arg His Arg Lys Glu Arg Arg Glu His
241 100 105 110
243 Val Cys Glu His Cys His Ser His Gly Met Gly His Asp Met Asn Ile
244 115 120 125
246 Glu Glu Lys Arg Ile Pro Ala Phe Leu Val Leu Ala Ile Leu Ile Val
247 130 135 140
249 Tyr Thr Ala Phe Gly Gly Val Leu Met Ser Lys Leu Glu Pro Trp Ser
250 145 150 155 160
252 Phe Phe Thr Ser Phe Tyr Trp Ser Phe Ile Thr Met Thr Thr Val Gly
253 165 170 175
255 Phe Gly Asp Leu Met Pro Arg Arg Asp Gly Tyr Met Tyr Ile Ile Leu
256 180 185 190
258 Leu Tyr Ile Ile Leu Gly Lys Phe Ser Met Lys Lys Lys Gln Lys Phe
259 195 200 205
261 Lys Ile Phe Leu Gly Leu Ala Ile Thr Thr Met Cys Ile Asp Leu Val
262 210 215 220
264 Gly Val Gln Tyr Ile Arg Lys Ile His Tyr Phe Gly Arg Lys Ile Gln

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RAW SEQUENCE LISTING

DATE: 11/13/2000

PATENT APPLICATION: US/08/816,011B

TIME: 13:15:25

Input Set : A:\Seq51.app

Output Set: N:\CRF3\11132000\H816011B.raw

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265 225          230          235          240
267 Asp Ala Arg Ser Ala Leu Ala Val Val Gly Gly Lys Val Val Leu Val
268          245          250          255
270 Ser Glu Leu Tyr Ala Asn Leu Met Gln Lys Arg Ala Arg Asn Met Ser
271          260          265          270
273 Arg Glu Ala Phe Ile Val Glu Asn Leu Tyr Val Ser Lys His Ile Ile
274          275          280          285
276 Pro Phe Ile Pro Thr Asp Ile Arg Cys Ile Arg Tyr Ile Asp Gln Thr
277          290          295          300
279 Ala Asp Ala Ala Thr Ile Ser Thr Ser Ser Ser Ala Ile Asp Met Gln
280 305          310          315          320
282 Ser Cys Arg Phe Cys His Ser Arg Tyr Ser Leu Asn Arg Ala Phe Lys
283          325          330          335
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290 <211> LENGTH: 51
291 <212> TYPE: DNA
292 <213> ORGANISM: Caenorhabditis elegans
294 <400> SEQUENCE: 5
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299 <211> LENGTH: 51
300 <212> TYPE: DNA
301 <213> ORGANISM: Caenorhabditis elegans
303 <400> SEQUENCE: 6
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308 <211> LENGTH: 24
309 <212> TYPE: PRT
310 <213> ORGANISM: Drosophila melanogaster
312 <400> SEQUENCE: 7
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316 Arg Cys Val Thr Asp Glu Cys Pro
317          20
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321 <211> LENGTH: 24
322 <212> TYPE: PRT
323 <213> ORGANISM: Drosophila melanogaster
325 <400> SEQUENCE: 8
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327 1          5          10          15
329 Arg Cys Val Thr Glu Gln Cys Ala
330          20
333 <210> SEQ ID NO: 9
334 <211> LENGTH: 24
335 <212> TYPE: PRT
336 <213> ORGANISM: Drosophila melanogaster
338 <400> SEQUENCE: 9
339 Ala Phe Leu Phe Phe Ile Glu Thr Glu Ala Thr Ile Gly Tyr Gly Tyr

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08/8/16, 011B 6

<210> 38
 <211> 337
 <212> PRT
 <213> Caenorhabditis elegans

See next page

<400> 38
 Met Ser Asp Gln Leu Phe Val Ala Phe Glu Lys Tyr Phe Leu Thr Ser
 1 5 10 15
 Asn Glu Val Lys Lys Asn Ala Ala Thr Glu Thr Trp Thr Phe Ser Ser
 20 25 30
 Ser Ile Phe Phe Ala Val Thr Val Val Thr Thr Ile Gly Tyr Gly Asn
 35 40 45
 Pro Val Pro Val Thr Asn Ile Gly Arg Ile Trp Cys Ile Leu Phe Ser
 50 55 60
 Leu Leu Gly Ile Pro Leu Thr Leu Val Thr Ile Ala Cys Leu Ala Gly
 65 70 75 80
 Lys Phe Leu Ser Glu His Leu Val Trp Leu Tyr Gly Asn Tyr Leu Lys
 85 90 95
 Leu Lys Tyr Leu Ile Leu Ser Arg His Arg Lys Glu Arg Arg Glu His
 100 105 110
 Val Cys Glu His Cys His Ser His Gly Met Gly His Asp Met Asn Ile
 115 120 125
 Glu Glu Lys Arg Ile Pro Ala Phe Leu Val Leu Ala Ile Leu Ile Val
 130 135 140
 Tyr Thr Ala Phe Gly Gly Val Leu Met Ser Lys Leu Glu Pro Trp Ser
 145 150 155 160
 Phe Phe Thr Ser Phe Tyr Trp Ser Phe Ile Thr Met Thr Thr Val Gly
 165 170 175
 Phe Gly Asp Leu Met Pro Arg Arg Asp Gly Tyr Met Tyr Ile Ile Leu
 180 185 190
 Leu Tyr Ile Ile Leu Gly Lys Phe Ser Met Lys Lys Lys Gln Lys Phe
 195 200 205
 Lys Ile Phe Leu Gly Leu Ala Ile Thr Thr Met Cys Ile Asp Leu Val
 210 215 220
 Gly Val Gln Tyr Ile Arg Lys Ile His Tyr Phe Gly Arg Lys Ile Gln
 225 230 235 240
 Asp Ala Arg Ser Ala Leu Ala Val Val Gly Gly Lys Val Val Leu Val
 245 250 255
 Ser Glu Leu Tyr Ala Asn Leu Met Gln Lys Arg Ala Arg Asn Met Ser
 260 265 270

08/816,011B 7

Arg Glu Ala Phe Ile Val Glu Asn Leu Tyr Val Ser Lys His Ile Ile
275 280 285

Pro Phe Ile Pro Thr Asp Ile Arg Cys Ile Arg Tyr Ile Asp Gln Thr
290 295 300

Ala Asp Ala Ala Thr Ile Ser Thr Ser Ser Ser Ala Ile Asp Met Gln
305 310 315 320

Ser Cys Arg Phe Cys His Ser Arg Tyr Ser Leu Asn Arg Ala Phe Lys
325 330 335

Xaa

see item 10 on Eva summary sheet

FYI

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

VERIFICATION SUMMARY

DATE: 11/13/2000

PATENT APPLICATION: US/08/816,011B

TIME: 13:15:26

Input Set : A:\Seq51.app

Output Set: N:\CRF3\11132000\H816011B.raw

L:829 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:38
L:829 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:38
L:829 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:38
L:829 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:38
L:829 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:38
L:843 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:39
L:843 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:39
L:843 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:39
L:989 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:46
L:989 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:46
L:989 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:46
L:989 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:46
L:989 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:46
L:1023 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:46
L:1023 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:46
L:1023 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:46
L:1023 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:46
M:340 Repeated in SeqNo=46
L:1024 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:46
L:1024 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:46
L:1024 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:46
L:1024 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:46
L:1073 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:51
L:1073 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:51
L:1073 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:51
L:1073 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:51
L:1073 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:51
L:1114 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:53
L:1114 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:53
L:1114 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:53
L:1114 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:53
L:1114 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:53
L:1119 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:53
L:1119 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:53
L:1119 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:53
L:1119 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:53
M:340 Repeated in SeqNo=53
L:1125 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:53
L:1125 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:53
L:1125 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:53
L:1125 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:53
L:1151 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:54
L:1151 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:54
L:1151 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:54
L:1151 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:54
L:1151 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:54
L:1261 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:56
L:1261 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:56

VERIFICATION SUMMARY

PATENT APPLICATION: US/08/816,011B

DATE: 11/13/2000

TIME: 13:15:26

Input Set : A:\Seq51.app

Output Set: N:\CRF3\11132000\H816011B.raw

L:1261 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:56
 L:1261 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:56
 L:1261 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:56
 L:1282 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:56
 L:1282 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:56
 L:1282 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:56
 L:1282 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:56
 M:340 Repeated in SeqNo=56
 L:1324 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:57
 L:1345 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:58
 L:1378 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:60
 L:1403 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:61
 L:1403 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:61
 L:1403 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:61
 L:1403 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:61
 L:1403 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:61
 L:1600 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:64